

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 05601, 10490
- (i) APPLICANT: Goodwin, Raymond G.
Smith, Craig A.
Armitage, Richard J.
Gruss, Hans-Jurgen
- (ii) TITLE OF INVENTION: Novel Cytokine That Binds CD30
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
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(F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: Apple Macintosh
(C) OPERATING SYSTEM: Apple 7.1
(D) SOFTWARE: Microsoft Word, Version 5.1a
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: --to be assigned--
(B) FILING DATE: 12 APRIL 1994
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/966,775
(B) FILING DATE: 27-OCT-1992
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 907,224
(B) FILING DATE: 01-JUL-1992
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 899,660
(B) FILING DATE: 15-JUN-1992
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 892,459
(B) FILING DATE: 02-JUN-1992
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 889,717
(B) FILING DATE: 26-MAY-1992
- (viii) ATTORNEY/AGENT INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1788 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: huCD30

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG	CGC	GTC	CTC	CTC	GCC	GCG	CTG	GGA	CTG	CTG	TTC	CTG	GGG	GCG	CTA	48
Met	Arg	Val	Leu	Leu	Ala	Ala	Leu	Gly	Leu	Leu	Phe	Leu	Gly	Ala	Leu	
1				5				10						15		
CGA	GCC	TTC	CCA	CAG	GAT	CGA	CCC	TTC	GAG	GAC	ACC	TGT	CAT	GGA	AAC	96
Arg	Ala	Phe	Pro	Gln	Asp	Arg	Pro	Phe	Glu	Asp	Thr	Cys	His	Gly	Asn	
			20					25					30			
CCC	AGC	CAC	TAC	TAT	GAC	AAG	GCT	GTC	AGG	AGG	TGC	TGT	TAC	CGC	TGC	144
Pro	Ser	His	Tyr	Tyr	Asp	Lys	Ala	Val	Arg	Arg	Cys	Cys	Tyr	Arg	Cys	
		35				40						45				
CCC	ATG	GGG	CTG	TTC	CCG	ACA	CAG	CAG	TGC	CCA	CAG	AGG	CCT	ACT	GAC	192
Pro	Met	Gly	Leu	Phe	Pro	Thr	Gln	Gln	Cys	Pro	Gln	Arg	Pro	Thr	Asp	
	50					55				60						
TGC	AGG	AAG	CAG	TGT	GAG	CCT	GAC	TAC	TAC	CTG	GAT	GAG	GCC	GAC	CGC	240
Cys	Arg	Lys	Gln	Cys	Glu	Pro	Asp	Tyr	Tyr	Leu	Asp	Glu	Ala	Asp	Arg	
65					70				75					80		
TGT	ACA	GCC	TGC	GTG	ACT	TGT	TCT	CGA	GAT	GAC	CTC	GTG	GAG	AAG	ACG	288
Cys	Thr	Ala	Cys	Val	Thr	Cys	Ser	Arg	Asp	Asp	Leu	Val	Glu	Lys	Thr	
			85					90						95		
CCG	TGT	GCA	TGG	AAC	TCC	TCC	CGT	GTC	TGC	GAA	TGT	CGA	CCC	GGC	ATG	336
Pro	Cys	Ala	Trp	Asn	Ser	Ser	Arg	Val	Cys	Glu	Cys	Arg	Pro	Gly	Met	
			100					105					110			

TTC	TGT	TCC	ACG	TCT	GCC	GTC	AAC	TCC	TGT	GCC	CGC	TGC	TTC	TTC	CAT	384
Phe	Cys	Ser	Thr	Ser	Ala	Val	Asn	Ser	Cys	Ala	Arg	Cys	Phe	Phe	His	
		115					120					125				
TCT	GTC	TGT	CCG	GCA	GGG	ATG	ATT	GTC	AAG	TTC	CCA	GGC	ACG	GCG	CAG	432
Ser	Val	Cys	Pro	Ala	Gly	Met	Ile	Val	Lys	Phe	Pro	Gly	Thr	Ala	Gln	
	130					135					140					
AAG	AAC	ACG	GTC	TGT	GAG	CCG	GCT	TCC	CCA	GGG	GTC	AGC	CCT	GCC	TGT	480
Lys	Asn	Thr	Val	Cys	Glu	Pro	Ala	Ser	Pro	Gly	Val	Ser	Pro	Ala	Cys	
145					150					155					160	
GCC	AGC	CCA	GAG	AAC	TGC	AAG	GAA	CCC	TCC	AGT	GGC	ACC	ATC	CCC	CAG	528
Ala	Ser	Pro	Glu	Asn	Cys	Lys	Glu	Pro	Ser	Ser	Gly	Thr	Ile	Pro	Gln	
				165					170					175		
GCC	AAG	CCC	ACC	CCG	GTG	TCC	CCA	GCA	ACC	TCC	AGT	GCC	AGC	ACC	ATG	576
Ala	Lys	Pro	Thr	Pro	Val	Ser	Pro	Ala	Thr	Ser	Ser	Ala	Ser	Thr	Met	
			180					185					190			
CCT	GTA	AGA	GGG	GGC	ACC	CGC	CTC	GCC	CAG	GAA	GCT	GCT	TCT	AAA	CTG	624
Pro	Val	Arg	Gly	Gly	Thr	Arg	Leu	Ala	Gln	Glu	Ala	Ala	Ser	Lys	Leu	
		195					200					205				
ACG	AGG	GCT	CCC	GAC	TCT	CCC	TCC	TCT	GTG	GGA	AGG	CCT	AGT	TCA	GAT	672
Thr	Arg	Ala	Pro	Asp	Ser	Pro	Ser	Ser	Val	Gly	Arg	Pro	Ser	Ser	Asp	
	210					215					220					
CCA	GGT	CTG	TCC	CCA	ACA	CAG	CCA	TGC	CCA	GAG	GGG	TCT	GGT	GAT	TGC	720
Pro	Gly	Leu	Ser	Pro	Thr	Gln	Pro	Cys	Pro	Glu	Gly	Ser	Gly	Asp	Cys	
225					230					235					240	
AGA	AAG	CAG	TGT	GAG	CCC	GAC	TAC	TAC	CTG	GAC	GAG	GCC	GGC	CGC	TGC	768
Arg	Lys	Gln	Cys	Glu	Pro	Asp	Tyr	Tyr	Leu	Asp	Glu	Ala	Gly	Arg	Cys	
				245					250					255		
ACA	GCC	TGC	GTG	AGC	TGT	TCT	CGA	GAT	GAC	CTT	GTG	GAG	AAG	ACG	CCA	816
Thr	Ala	Cys	Val	Ser	Cys	Ser	Arg	Asp	Asp	Leu	Val	Glu	Lys	Thr	Pro	
			260					265					270			
TGT	GCA	TGG	AAC	TCC	TCC	CGC	ACC	TGC	GAA	TGT	CGA	CCT	GGC	ATG	ATC	864
Cys	Ala	Trp	Asn	Ser	Ser	Arg	Thr	Cys	Glu	Cys	Arg	Pro	Gly	Met	Ile	
		275					280					285				
TGT	GCC	ACA	TCA	GCC	ACC	AAC	TCC	TGT	GCC	CGC	TGT	GTC	CCC	TAC	CCA	912
Cys	Ala	Thr	Ser	Ala	Thr	Asn	Ser	Cys	Ala	Arg	Cys	Val	Pro	Tyr	Pro	
	290					295					300					
ATC	TGT	GCA	GGA	GAG	ACG	GTC	ACC	AAG	CCC	CAG	GAT	ATG	GCT	GAG	AAG	960
Ile	Cys	Ala	Gly	Glu	Thr	Val	Thr	Lys	Pro	Gln	Asp	Met	Ala	Glu	Lys	
305					310					315					320	
GAC	ACC	ACC	TTT	GAG	GCG	CCA	CCC	CTG	GGG	ACC	CAG	CCG	GAC	TGC	AAC	1008
Asp	Thr	Thr	Phe	Glu	Ala	Pro	Pro	Leu	Gly	Thr	Gln	Pro	Asp	Cys	Asn	
				325					330					335		
CCC	ACC	CCA	GAG	AAT	GGC	GAG	GCG	CCT	GCC	AGC	ACC	AGC	CCC	ACT	CAG	1056
Pro	Thr	Pro	Glu	Asn	Gly	Glu	Ala	Pro	Ala	Ser	Thr	Ser	Pro	Thr	Gln	
			340					345					350			

AGC	TTG	CTG	GTG	GAC	TCC	CAG	GCC	AGT	AAG	ACG	CTG	CCC	ATC	CCA	ACC	1104
Ser	Leu	Leu	Val	Asp	Ser	Gln	Ala	Ser	Lys	Thr	Leu	Pro	Ile	Pro	Thr	
		355					360					365				
AGC	GCT	CCC	GTC	GCT	CTC	TCC	TCC	ACG	GGG	AAG	CCC	GTT	CTG	GAT	GCA	1152
Ser	Ala	Pro	Val	Ala	Leu	Ser	Ser	Thr	Gly	Lys	Pro	Val	Leu	Asp	Ala	
	370					375					380					
GGG	CCA	GTG	CTC	TTC	TGG	GTG	ATC	CTG	GTG	TTG	GTT	GTG	GTG	GTC	GGC	1200
Gly	Pro	Val	Leu	Phe	Trp	Val	Ile	Leu	Val	Leu	Val	Val	Val	Val	Gly	
	385				390					395					400	
TCC	AGC	GCC	TTC	CTC	CTG	TGC	CAC	CGG	AGG	GCC	TGC	AGG	AAG	CGA	ATT	1248
Ser	Ser	Ala	Phe	Leu	Leu	Cys	His	Arg	Arg	Ala	Cys	Arg	Lys	Arg	Ile	
			405					410						415		
CGG	CAG	AAG	CTC	CAC	CTG	TGC	TAC	CCG	GTC	CAG	ACC	TCC	CAG	CCC	AAG	1296
Arg	Gln	Lys	Leu	His	Leu	Cys	Tyr	Pro	Val	Gln	Thr	Ser	Gln	Pro	Lys	
		420						425					430			
CTA	GAG	CTT	GTG	GAT	TCC	AGA	CCC	AGG	AGG	AGC	TCA	ACG	CAG	CTG	AGG	1344
Leu	Glu	Leu	Val	Asp	Ser	Arg	Pro	Arg	Arg	Ser	Ser	Thr	Gln	Leu	Arg	
		435					440					445				
AGT	GGT	GCG	TCG	GTG	ACA	GAA	CCC	GTC	GCG	GAA	GAG	CGA	GGG	TTA	ATG	1392
Ser	Gly	Ala	Ser	Val	Thr	Glu	Pro	Val	Ala	Glu	Glu	Arg	Gly	Leu	Met	
	450					455					460					
AGC	CAG	CCA	CTG	ATG	GAG	ACC	TGC	CAC	AGC	GTG	GGG	GCA	GCC	TAC	CTG	1440
Ser	Gln	Pro	Leu	Met	Glu	Thr	Cys	His	Ser	Val	Gly	Ala	Ala	Tyr	Leu	
	465				470					475					480	
GAG	AGC	CTG	CCG	CTG	CAG	GAT	GCC	AGC	CCG	GCC	GGG	GGC	CCC	TCG	TCC	1488
Glu	Ser	Leu	Pro	Leu	Gln	Asp	Ala	Ser	Pro	Ala	Gly	Gly	Pro	Ser	Ser	
			485						490					495		
CCC	AGG	GAC	CTT	CCT	GAG	CCC	CGG	GTG	TCC	ACG	GAG	CAC	ACC	AAT	AAC	1536
Pro	Arg	Asp	Leu	Pro	Glu	Pro	Arg	Val	Ser	Thr	Glu	His	Thr	Asn	Asn	
		500						505					510			
AAG	ATT	GAG	AAA	ATC	TAC	ATC	ATG	AAG	GCT	GAC	ACC	GTG	ATC	GTG	GGG	1584
Lys	Ile	Glu	Lys	Ile	Tyr	Ile	Met	Lys	Ala	Asp	Thr	Val	Ile	Val	Gly	
		515					520					525				
ACC	GTG	AAG	GCT	GAG	CTG	CCG	GAG	GGC	CGG	GGC	CTG	GCG	GGG	CCA	GCA	1632
Thr	Val	Lys	Ala	Glu	Leu	Pro	Glu	Gly	Arg	Gly	Leu	Ala	Gly	Pro	Ala	
	530					535					540					
GAG	CCC	GAG	TTG	GAG	GAG	GAG	CTG	GAG	GCG	GAC	CAT	ACC	CCC	CAC	TAC	1680
Glu	Pro	Glu	Leu	Glu	Glu	Glu	Leu	Glu	Ala	Asp	His	Thr	Pro	His	Tyr	
	545				550					555					560	
CCC	GAG	CAG	GAG	ACA	GAA	CCG	CCT	CTG	GGC	AGC	TGC	AGC	GAT	GTC	ATG	1728
Pro	Glu	Gln	Glu	Thr	Glu	Pro	Pro	Leu	Gly	Ser	Cys	Ser	Asp	Val	Met	
				565					570					575		
CTC	TCA	GTG	GAA	GAG	GAA	GGG	AAA	GAA	GAC	CCC	TTG	CCC	ACA	GCT	GCC	1776
Leu	Ser	Val	Glu	Glu	Glu	Gly	Lys	Glu	Asp	Pro	Leu	Pro	Thr	Ala	Ala	
			580					585					590			

52

TCT GGA AAG TGA
Ser Gly Lys
595

1788

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Val Leu Leu Ala Ala Leu Gly Leu Leu Phe Leu Gly Ala Leu
1 5 10 15
Arg Ala Phe Pro Gln Asp Arg Pro Phe Glu Asp Thr Cys His Gly Asn
20 25 30
Pro Ser His Tyr Tyr Asp Lys Ala Val Arg Arg Cys Cys Tyr Arg Cys
35 40 45
Pro Met Gly Leu Phe Pro Thr Gln Gln Cys Pro Gln Arg Pro Thr Asp
50 55 60
Cys Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Asp Arg
65 70 75 80
Cys Thr Ala Cys Val Thr Cys Ser Arg Asp Asp Leu Val Glu Lys Thr
85 90 95
Pro Cys Ala Trp Asn Ser Ser Arg Val Cys Glu Cys Arg Pro Gly Met
100 105 110
Phe Cys Ser Thr Ser Ala Val Asn Ser Cys Ala Arg Cys Phe Phe His
115 120 125
Ser Val Cys Pro Ala Gly Met Ile Val Lys Phe Pro Gly Thr Ala Gln
130 135 140
Lys Asn Thr Val Cys Glu Pro Ala Ser Pro Gly Val Ser Pro Ala Cys
145 150 155 160
Ala Ser Pro Glu Asn Cys Lys Glu Pro Ser Ser Gly Thr Ile Pro Gln
165 170 175
Ala Lys Pro Thr Pro Val Ser Pro Ala Thr Ser Ser Ala Ser Thr Met
180 185 190
Pro Val Arg Gly Gly Thr Arg Leu Ala Gln Glu Ala Ala Ser Lys Leu
195 200 205
Thr Arg Ala Pro Asp Ser Pro Ser Ser Val Gly Arg Pro Ser Ser Asp
210 215 220
Pro Gly Leu Ser Pro Thr Gln Pro Cys Pro Glu Gly Ser Gly Asp Cys
225 230 235 240

Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Gly Arg Cys
 245 250 255
 Thr Ala Cys Val Ser Cys Ser Arg Asp Asp Leu Val Glu Lys Thr Pro
 260 265 270
 Cys Ala Trp Asn Ser Ser Arg Thr Cys Glu Cys Arg Pro Gly Met Ile
 275 280 285
 Cys Ala Thr Ser Ala Thr Asn Ser Cys Ala Arg Cys Val Pro Tyr Pro
 290 295 300
 Ile Cys Ala Gly Glu Thr Val Thr Lys Pro Gln Asp Met Ala Glu Lys
 305 310 315 320
 Asp Thr Thr Phe Glu Ala Pro Pro Leu Gly Thr Gln Pro Asp Cys Asn
 325 330 335
 Pro Thr Pro Glu Asn Gly Glu Ala Pro Ala Ser Thr Ser Pro Thr Gln
 340 345 350
 Ser Leu Leu Val Asp Ser Gln Ala Ser Lys Thr Leu Pro Ile Pro Thr
 355 360 365
 Ser Ala Pro Val Ala Leu Ser Ser Thr Gly Lys Pro Val Leu Asp Ala
 370 375 380
 Gly Pro Val Leu Phe Trp Val Ile Leu Val Leu Val Val Val Val Gly
 385 390 395 400
 Ser Ser Ala Phe Leu Leu Cys His Arg Arg Ala Cys Arg Lys Arg Ile
 405 410 415
 Arg Gln Lys Leu His Leu Cys Tyr Pro Val Gln Thr Ser Gln Pro Lys
 420 425 430
 Leu Glu Leu Val Asp Ser Arg Pro Arg Arg Ser Ser Thr Gln Leu Arg
 435 440 445
 Ser Gly Ala Ser Val Thr Glu Pro Val Ala Glu Glu Arg Gly Leu Met
 450 455 460
 Ser Gln Pro Leu Met Glu Thr Cys His Ser Val Gly Ala Ala Tyr Leu
 465 470 475 480
 Glu Ser Leu Pro Leu Gln Asp Ala Ser Pro Ala Gly Gly Pro Ser Ser
 485 490 495
 Pro Arg Asp Leu Pro Glu Pro Arg Val Ser Thr Glu His Thr Asn Asn
 500 505 510
 Lys Ile Glu Lys Ile Tyr Ile Met Lys Ala Asp Thr Val Ile Val Gly
 515 520 525
 Thr Val Lys Ala Glu Leu Pro Glu Gly Arg Gly Leu Ala Gly Pro Ala
 530 535 540
 Glu Pro Glu Leu Glu Glu Glu Leu Glu Ala Asp His Thr Pro His Tyr
 545 550 555 560

Pro Glu Gln Glu Thr Glu Pro Pro Leu Gly Ser Cys Ser Asp Val Met
565 570 575

Leu Ser Val Glu Glu Glu Gly Lys Glu Asp Pro Leu Pro Thr Ala Ala
580 585 590

Ser Gly Lys
595

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 699 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: hIgG1Fc

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAG CCC AGA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA	48
Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala	
1 5 10 15	
CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC	96
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro	
20 25 30	
AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG	144
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val	
35 40 45	
GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG	192
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val	
50 55 60	
GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG	240
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln	
65 70 75 80	
TAC AAC AGC ACG TAC CGG GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG	288
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln	
85 90 95	

55

GAC TGG CTG AAT GGC AAG GAC TAC AAG TGC AAG GTC TCC AAC AAA GCC	336
Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala	
100 105 110	
CTC CCA GCC CCC ATG CAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC	384
Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro	
115 120 125	
CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC	432
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr	
130 135 140	
AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGG	480
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg	
145 150 155 160	
CAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC	528
His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr	
165 170 175	
AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC	576
Lys Thr Thr Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr	
180 185 190	
AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC	624
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe	
195 200 205	
TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG	672
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys	
210 215 220	
AGC CTC TCC CTG TCT CCG GGT AAA TGA	699
Ser Leu Ser Leu Ser Pro Gly Lys	
225 230	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala	
1 5 10 15	
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro	
20 25 30	
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val	
35 40 45	
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val	
50 55 60	

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95
 Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110
 Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg
 145 150 155 160
 His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220
 Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: muCD30-L

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GAG CCA GGG CTG CAA CAA GCA GGC AGC TGT GGG GCT CCT TCC CCT
 Met Glu Pro Gly Leu Gln Gln Ala Gly Ser Cys Gly Ala Pro Ser Pro
 1 5 10 15

48

GAC CCA GCC ATG CAG GTG CAG CCC GGC TCG GTA GCC AGC CCC TGG AGA	96
Asp Pro Ala Met Gln Val Gln Pro Gly Ser Val Ala Ser Pro Trp Arg	
20 25 30	
AGC ACG AGG CCC TGG AGA AGC ACA AGT CGC AGC TAC TTC TAC CTC AGC	144
Ser Thr Arg Pro Trp Arg Ser Thr Ser Arg Ser Tyr Phe Tyr Leu Ser	
35 40 45	
ACC ACC GCA CTG GTG TGC CTT GTT GTG GCA GTG GCG ATC ATT CTG GTA	192
Thr Thr Ala Leu Val Cys Leu Val Val Ala Val Ala Ile Ile Leu Val	
50 55 60	
CTG GTA GTC CAG AAA AAG GAC TCC ACT CCA AAT ACA ACT GAG AAG GCC	240
Leu Val Val Gln Lys Lys Asp Ser Thr Pro Asn Thr Thr Glu Lys Ala	
65 70 75 80	
CCC CTT AAA GGA GGA AAT TGC TCA GAG GAT CTC TTC TGT ACC CTG AAA	288
Pro Leu Lys Gly Gly Asn Cys Ser Glu Asp Leu Phe Cys Thr Leu Lys	
85 90 95	
AGT ACT CCA TCC AAG AAG TCA TGG GCC TAC CTC CAA GTG TCA AAG CAT	336
Ser Thr Pro Ser Lys Lys Ser Trp Ala Tyr Leu Gln Val Ser Lys His	
100 105 110	
CTC AAC AAT ACC AAA CTG TCA TGG AAC GAA GAT GGC ACC ATC CAC GGA	384
Leu Asn Asn Thr Lys Leu Ser Trp Asn Glu Asp Gly Thr Ile His Gly	
115 120 125	
CTC ATA TAC CAG GAC GGG AAC CTG ATA GTC CAA TTC CCT GGC TTG TAC	432
Leu Ile Tyr Gln Asp Gly Asn Leu Ile Val Gln Phe Pro Gly Leu Tyr	
130 135 140	
TTC ATC GTT TGC CAA CTG CAG TTC CTC GTG CAG TGC TCA AAT CAT TCT	480
Phe Ile Val Cys Gln Leu Gln Phe Leu Val Gln Cys Ser Asn His Ser	
145 150 155 160	
GTG GAC CTG ACA TTG CAG CTC CTC ATC AAT TCC AAG ATC AAA AAG CAG	528
Val Asp Leu Thr Leu Gln Leu Leu Ile Asn Ser Lys Ile Lys Lys Gln	
165 170 175	
ACG TTG GTA ACA GTG TGT GAG TCT GGA GTT CAG AGT AAG AAC ATC TAC	576
Thr Leu Val Thr Val Cys Glu Ser Gly Val Gln Ser Lys Asn Ile Tyr	
180 185 190	
CAG AAT CTC TCT CAG TTT TTG CTG CAT TAC TTA CAG GTC AAC TCT ACC	624
Gln Asn Leu Ser Gln Phe Leu Leu His Tyr Leu Gln Val Asn Ser Thr	
195 200 205	
ATA TCA GTC AGG GTG GAT AAT TTC CAG TAT GTG GAT ACA AAC ACT TTC	672
Ile Ser Val Arg Val Asp Asn Phe Gln Tyr Val Asp Thr Asn Thr Phe	
210 215 220	
CCT CTT GAT AAT GTG CTA TCC GTC TTC TTA TAT AGT AGC TCA GAC TGA	720
Pro Leu Asp Asn Val Leu Ser Val Phe Leu Tyr Ser Ser Ser Asp	
225 230 235 240	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Pro Gly Leu Gln Gln Ala Gly Ser Cys Gly Ala Pro Ser Pro
1 5 10 15
Asp Pro Ala Met Gln Val Gln Pro Gly Ser Val Ala Ser Pro Trp Arg
20 25 30
Ser Thr Arg Pro Trp Arg Ser Thr Ser Arg Ser Tyr Phe Tyr Leu Ser
35 40 45
Thr Thr Ala Leu Val Cys Leu Val Val Ala Val Ala Ile Ile Leu Val
50 55 60
Leu Val Val Gln Lys Lys Asp Ser Thr Pro Asn Thr Thr Glu Lys Ala
65 70 75 80
Pro Leu Lys Gly Gly Asn Cys Ser Glu Asp Leu Phe Cys Thr Leu Lys
85 90 95
Ser Thr Pro Ser Lys Lys Ser Trp Ala Tyr Leu Gln Val Ser Lys His
100 105 110
Leu Asn Asn Thr Lys Leu Ser Trp Asn Glu Asp Gly Thr Ile His Gly
115 120 125
Leu Ile Tyr Gln Asp Gly Asn Leu Ile Val Gln Phe Pro Gly Leu Tyr
130 135 140
Phe Ile Val Cys Gln Leu Gln Phe Leu Val Gln Cys Ser Asn His Ser
145 150 155 160
Val Asp Leu Thr Leu Gln Leu Leu Ile Asn Ser Lys Ile Lys Lys Gln
165 170 175
Thr Leu Val Thr Val Cys Glu Ser Gly Val Gln Ser Lys Asn Ile Tyr
180 185 190
Gln Asn Leu Ser Gln Phe Leu Leu His Tyr Leu Gln Val Asn Ser Thr
195 200 205
Ile Ser Val Arg Val Asp Asn Phe Gln Tyr Val Asp Thr Asn Thr Phe
210 215 220
Pro Leu Asp Asn Val Leu Ser Val Phe Leu Tyr Ser Ser Ser Asp
225 230 235

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 705 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: huCD30-L

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GAC CCA GGG CTG CAG CAA GCA CTC AAC GGA ATG GCC CCT CCT GGA	48
Met Asp Pro Gly Leu Gln Gln Ala Leu Asn Gly Met Ala Pro Pro Gly	
1 5 10 15	
GAC ACA GCC ATG CAT GTG CCG GCG GGC TCC GTG GCC AGC CAC CTG GGG	96
Asp Thr Ala Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly	
20 25 30	
ACC ACG AGC CGC AGC TAT TTC TAT TTG ACC ACA GCC ACT CTG GCT CTG	144
Thr Thr Ser Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu	
35 40 45	
TGC CTT GTC TTC ACG GTG GCC ACT ATT ATG GTG TTG GTC GTT CAG AGG	192
Cys Leu Val Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg	
50 55 60	
ACG GAC TCC ATT CCC AAC TCA CCT GAC AAC GTC CCC CTC AAA GGA GGA	240
Thr Asp Ser Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly	
65 70 75 80	
AAT TGC TCA GAA GAC CTC TTA TGT ATC CTG AAA AGA GCT CCA TTC AAG	288
Asn Cys Ser Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys	
85 90 95	
AAG TCA TGG GCC TAC CTC CAA GTG GCA AAG CAT CTA AAC AAA ACC AAG	336
Lys Ser Trp Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys	
100 105 110	
TTG TCT TGG AAC AAA GAT GGC ATT CTC CAT GGA GTC AGA TAT CAG GAT	384
Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp	
115 120 125	
GGG AAT CTG GTG ATC CAA TTC CCT GGT TTG TAC TTC ATC ATT TGC CAA	432
Gly Asn Leu Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln	
130 135 140	
CTG CAG TTT CTT GTA CAA TGC CCA AAT AAT TCT GTC GAT CTG AAG TTG	480
Leu Gln Phe Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu Lys Leu	
145 150 155 160	

GAG CTT CTC ATC AAC AAG CAT ATC AAA AAA CAG GCC CTG GTG ACA GTG	528
Glu Leu Leu Ile Asn Lys His Ile Lys Lys Gln Ala Leu Val Thr Val	
165 170 175	
TGT GAG TCT GGA ATG CAA ACG AAA CAC GTA TAC CAG AAT CTC TCT CAA	576
Cys Glu Ser Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln	
180 185 190	
TTC TTG CTG GAT TAC CTG CAG GTC AAC ACC ACC ATA TCA GTC AAT GTG	624
Phe Leu Leu Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val	
195 200 205	
GAT ACA TTC CAG TAC ATA GAT ACA AGC ACC TTT CCT CTT GAG AAT GTG	672
Asp Thr Phe Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val	
210 215 220	
TTG TCC ATC TTC TTA TAC AGT AAT TCA GAC TGA	705
Leu Ser Ile Phe Leu Tyr Ser Asn Ser Asp	
225 230 235	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Pro Gly Leu Gln Gln Ala Leu Asn Gly Met Ala Pro Pro Gly	
1 5 10 15	
Asp Thr Ala Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly	
20 25 30	
Thr Thr Ser Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu	
35 40 45	
Cys Leu Val Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg	
50 55 60	
Thr Asp Ser Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly	
65 70 75 80	
Asn Cys Ser Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys	
85 90 95	
Lys Ser Trp Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys	
100 105 110	
Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp	
115 120 125	
Gly Asn Leu Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln	
130 135 140	

Leu Gln Phe Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu Lys Leu
 145 150 155 160
 Glu Leu Leu Ile Asn Lys His Ile Lys Lys Gln Ala Leu Val Thr Val
 165 170 175
 Cys Glu Ser Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln
 180 185 190
 Phe Leu Leu Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val
 195 200 205
 Asp Thr Phe Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val
 210 215 220
 Leu Ser Ile Phe Leu Tyr Ser Asn Ser Asp
 225 230

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 5' PCR Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATAGCGGCCG CCACCATGCG CGTCCTCCTC GCCGCGCTG

39

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 3' PCR Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACAAGATCTG GGCTCCTTCC CCGTGGAGGA GAGAGCGAC

39

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid

62

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: BGL II Adaptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATCTGGCAA CGAAGGTACC ATGG

24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: BGL II Adaptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCATGGTACC TTCGTTGCCA

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: Upstream sequence

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG GGC TGT GGG GCT CCT TCC CCT GAC CCA GCC
Met Gly Cys Gly Ala Pro Ser Pro Asp Pro Ala
1 5 10

33

[illegible]

(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gly Cys Gly Ala Pro Ser Pro Asp Pro Ala
1 5 10

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: FLAG peptide

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: Murine cDNA Primer

AGATGCTTTG ACACTTG

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (vii) IMMEDIATE SOURCE:
(B) CLONE: Human cDNA Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATCACCAGAT TCCCATC

17

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 663 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vii) IMMEDIATE SOURCE:
(B) CLONE: muCD30-L

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATG CAG GTG CAG CCC GGC TCG GTA GCC AGC CCC TGG AGA AGC ACG AGG	48
Met Gln Val Gln Pro Gly Ser Val Ala Ser Pro Trp Arg Ser Thr Arg	
1 5 10 15	
CCC TGG AGA AGC ACA AGT CGC AGC TAC TTC TAC CTC AGC ACC ACC GCA	96
Pro Trp Arg Ser Thr Ser Arg Ser Tyr Phe Tyr Leu Ser Thr Thr Ala	
20 25 30	
CTG GTG TGC CTT GTT GTG GCA GTG GCG ATC ATT CTG GTA CTG GTA GTC	144
Leu Val Cys Leu Val Val Ala Val Ala Ile Ile Leu Val Leu Val Val	
35 40 45	

CAG AAA AAG GAC TCC ACT CCA AAT ACA ACT GAG AAG GCC CCC CTT AAA	192
Gln Lys Lys Asp Ser Thr Pro Asn Thr Thr Glu Lys Ala Pro Leu Lys	
50 55 60	
GGA GGA AAT TGC TCA GAG GAT CTC TTC TGT ACC CTG AAA AGT ACT CCA	240
Gly Gly Asn Cys Ser Glu Asp Leu Phe Cys Thr Leu Lys Ser Thr Pro	
65 70 75 80	
TCC AAG AAG TCA TGG GCC TAC CTC CAA GTG TCA AAG CAT CTC AAC AAT	288
Ser Lys Lys Ser Trp Ala Tyr Leu Gln Val Ser Lys His Leu Asn Asn	
85 90 95	
ACC AAA CTG TCA TGG AAC GAA GAT GGC ACC ATC CAC GGA CTC ATA TAC	336
Thr Lys Leu Ser Trp Asn Glu Asp Gly Thr Ile His Gly Leu Ile Tyr	
100 105 110	
CAG GAC GGG AAC CTG ATA GTC CAA TTC CCT GGC TTG TAC TTC ATC GTT	384
Gln Asp Gly Asn Leu Ile Val Gln Phe Pro Gly Leu Tyr Phe Ile Val	
115 120 125	
TGC CAA CTG CAG TTC CTC GTG CAG TGC TCA AAT CAT TCT GTG GAC CTG	432
Cys Gln Leu Gln Phe Leu Val Gln Cys Ser Asn His Ser Val Asp Leu	
130 135 140	
ACA TTG CAG CTC CTC ATC AAT TCC AAG ATC AAA AAG CAG ACG TTG GTA	480
Thr Leu Gln Leu Leu Ile Asn Ser Lys Ile Lys Lys Gln Thr Leu Val	
145 150 155 160	
ACA GTG TGT GAG TCT GGA GTT CAG AGT AAG AAC ATC TAC CAG AAT CTC	528
Thr Val Cys Glu Ser Gly Val Gln Ser Lys Asn Ile Tyr Gln Asn Leu	
165 170 175	
TCT CAG TTT TTG CTG CAT TAC TTA CAG GTC AAC TCT ACC ATA TCA GTC	576
Ser Gln Phe Leu Leu His Tyr Leu Gln Val Asn Ser Thr Ile Ser Val	
180 185 190	
AGG GTG GAT AAT TTC CAG TAT GTG GAT ACA AAC ACT TTC CCT CTT GAT	624
Arg Val Asp Asn Phe Gln Tyr Val Asp Thr Asn Thr Phe Pro Leu Asp	
195 200 205	
AAT GTG CTA TCC GTC TTC TTA TAT AGT AGC TCA GAC TGA	663
Asn Val Leu Ser Val Phe Leu Tyr Ser Ser Ser Asp	
210 215 220	

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Gln	Val	Gln	Pro	Gly	Ser	Val	Ala	Ser	Pro	Trp	Arg	Ser	Thr	Arg
1				5					10					15	

Pro Trp Arg Ser Thr Ser Arg Ser Tyr Phe Tyr Leu Ser Thr Thr Ala
 20 25 30
 Leu Val Cys Leu Val Val Ala Val Ala Ile Ile Leu Val Leu Val Val
 35 40 45
 Gln Lys Lys Asp Ser Thr Pro Asn Thr Thr Glu Lys Ala Pro Leu Lys
 50 55 60
 Gly Gly Asn Cys Ser Glu Asp Leu Phe Cys Thr Leu Lys Ser Thr Pro
 65 70 75 80
 Ser Lys Lys Ser Trp Ala Tyr Leu Gln Val Ser Lys His Leu Asn Asn
 85 90 95
 Thr Lys Leu Ser Trp Asn Glu Asp Gly Thr Ile His Gly Leu Ile Tyr
 100 105 110
 Gln Asp Gly Asn Leu Ile Val Gln Phe Pro Gly Leu Tyr Phe Ile Val
 115 120 125
 Cys Gln Leu Gln Phe Leu Val Gln Cys Ser Asn His Ser Val Asp Leu
 130 135 140
 Thr Leu Gln Leu Leu Ile Asn Ser Lys Ile Lys Lys Gln Thr Leu Val
 145 150 155 160
 Thr Val Cys Glu Ser Gly Val Gln Ser Lys Asn Ile Tyr Gln Asn Leu
 165 170 175
 Ser Gln Phe Leu Leu His Tyr Leu Gln Val Asn Ser Thr Ile Ser Val
 180 185 190
 Arg Val Asp Asn Phe Gln Tyr Val Asp Thr Asn Thr Phe Pro Leu Asp
 195 200 205
 Asn Val Leu Ser Val Phe Leu Tyr Ser Ser Ser Asp
 210 215 220

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein fragment
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: huCD30 fragment (PRELIM)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Pro Gly Asp Thr Val Xaa His Val Pro Ala Gly Ser Glu Ala Ser His
 1 5 10 15
 Leu Gly Thr Thr Ser Arg Xaa Tyr Phe Tyr Leu Thr Thr Xaa Thr Leu
 20 25 30
 Ala Leu Cys Leu Val Phe Thr Val Ala Thr Ile Met Val Leu Val Val
 35 40 45
 Gln Arg Thr Asp Ser Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys
 50 55 60
 Gly Gly Asn Cys Ser Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro
 65 70 75 80
 Phe Lys Lys Ser Trp Ala Tyr Leu Gln Val Xaa Lys His Leu Asn Lys
 85 90 95
 Thr Xaa Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr
 100 105 110
 Gln Asp Gly Asn Leu Val Ile Gln Phe Pro Gly Phe Val
 115 120 125

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein fragment

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: muCD30 fragment (PRELIM)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Gln Val Gln Pro Gly Ser Val Ala Ser Pro Trp Arg Ser Thr Arg
 1 5 10 15
 Pro Trp Arg Ser Thr Ser Arg Ser Tyr Phe Tyr Leu Ser Thr Thr Ala
 20 25 30
 Leu Val Cys Leu Val Val Xaa Val Ala Ile Ile Leu Val Leu Val Val
 35 40 45
 Gln Lys Lys Asp Ser Thr Pro Asn Thr Thr Glu Lys Ala Pro Leu Lys
 50 55 60
 Gly Gly Asn Cys Ser Glu Asp Leu Phe Cys Thr Leu Lys Ser Thr Pro
 65 70 75 80

Ser Lys Lys Ser Trp Ala Tyr Leu Gln Val Ser Lys His Leu Asn Asn
85 90 95

Thr Lys Leu Ser Trp Asn Glu Asp Gly Thr Ile His Gly Leu Ile Tyr
100 105 110

Gln Asp Gly Asn Leu Ile Val Gln Phe Pro Gly Leu Tyr Phe Ile Val
115 120 125

Cys Gln
130

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 648 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: huCD30-L

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATG CAT GTG CCG GCG GGC TCC GTG GCC AGC CAC CTG GGG ACC ACG AGC	48
Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly Thr Thr Ser	
1 5 10 15	
CGC AGC TAT TTC TAT TTG ACC ACA GCC ACT CTG GCT CTG TGC CTT GTC	96
Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu Cys Leu Val	
20 25 30	
TTC ACG GTG GCC ACT ATT ATG GTG TTG GTC GTT CAG AGG ACG GAC TCC	144
Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg Thr Asp Ser	
35 40 45	
ATT CCC AAC TCA CCT GAC AAC GTC CCC CTC AAA GGA GGA AAT TGC TCA	192
Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly Asn Cys Ser	
50 55 60	
GAA GAC CTC TTA TGT ATC CTG AAA AGA GCT CCA TTC AAG AAG TCA TGG	240
Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys Lys Ser Trp	
65 70 75 80	
GCC TAC CTC CAA GTG GCA AAG CAT CTA AAC AAA ACC AAG TTG TCT TGG	288
Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys Leu Ser Trp	
85 90 95	

AAC AAA GAT GGC ATT CTC CAT GGA GTC AGA TAT CAG GAT GGG AAT CTG	336
Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp Gly Asn Leu	
100 105 110	
GTG ATC CAA TTC CCT GGT TTG TAC TTC ATC ATT TGC CAA CTG CAG TTT	384
Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln Leu Gln Phe	
115 120 125	
CTT GTA CAA TGC CCA AAT AAT TCT GTC GAT CTG AAG TTG GAG CTT CTC	432
Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu Lys Leu Glu Leu Leu	
130 135 140	
ATC AAC AAG CAT ATC AAA AAA CAG GCC CTG GTG ACA GTG TGT GAG TCT	480
Ile Asn Lys His Ile Lys Lys Gln Ala Leu Val Thr Val Cys Glu Ser	
145 150 155 160	
GGA ATG CAA ACG AAA CAC GTA TAC CAG AAT CTC TCT CAA TTC TTG CTG	528
Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln Phe Leu Leu	
165 170 175	
GAT TAC CTG CAG GTC AAC ACC ACC ATA TCA GTC AAT GTG GAT ACA TTC	576
Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val Asp Thr Phe	
180 185 190	
CAG TAC ATA GAT ACA AGC ACC TTT CCT CTT GAG AAT GTG TTG TCC ATC	624
Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val Leu Ser Ile	
195 200 205	
TTC TTA TAC AGT AAT TCA GAC TGA	648
Phe Leu Tyr Ser Asn Ser Asp	
210 215	

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly Thr Thr Ser	
1 5 10 15	
Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu Cys Leu Val	
20 25 30	
Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg Thr Asp Ser	
35 40 45	
Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly Asn Cys Ser	
50 55 60	
Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys Lys Ser Trp	
65 70 75 80	

Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys Leu Ser Trp
 85 90 95
 Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp Gly Asn Leu
 100 105 110
 Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln Leu Gln Phe
 115 120 125
 Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu Lys Leu Glu Leu Leu
 130 135 140
 Ile Asn Lys His Ile Lys Lys Gln Ala Leu Val Thr Val Cys Glu Ser
 145 150 155 160
 Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln Phe Leu Leu
 165 170 175
 Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val Asp Thr Phe
 180 185 190
 Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val Leu Ser Ile
 195 200 205
 Phe Leu Tyr Ser Asn Ser Asp
 210 215